

FIGURE 1A

970 990 1010
 TGACCCCCACCACCGGCCACCCATCTGTCAACCTTGACAGCGCCCACACCCCTCTAGCAC
 T P P P A T H L S P L D S A H T L L A P

 1030 1050 1070
 CTCCTGACAGCAGTGAAGAAGATCTGCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTG
 P D S S E K I C T V Q L V G N S W T P G

 1090 1110 1130
 GCTACCCCGAGACCCAGGAGGCCCTGCCCCCAGGTGACATGGTCTGGGACAGCTG
 Y P E T Q E A L C P Q V T W S W D Q L P

 1150 1170 1190
 CCAGCAGAGCTCTGGCCCCGCTGCTGCGCCACACTCTGCCAGAGTCCCCAGCCGGCT
 S R A L G P A A A P T L S P E S P A G S

 1210 1230 1250
 CGCCAGCCATGATGCTGCAGCCGGCCCGCAGCTCTACGACGTGATGGACGGCGGTCCCAG
 P A M M L Q P G P Q L Y D V M D A Y P A

 1270 1290 1310
 CGCGGGCGCTGGAAGGAGTTCTGTGCGCACGCTGGGGCTGCGCGAGGCAGAGATCGAACCG
 R R W K E F V R T L G L R E A E I E A V

 1330 1350 1370
 TGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGGCC
 E V E I G R F R D O O Y E M L K R W R Q

 1390 1410 1430
 AGCAGCAGCCCGCGGGCTCGGAGCCGTTACGCGGCCCTGGAGCGCATGGGGCTGGACG
 Q O P A G L G A V Y A A L E R M G L D G

 1450 1470 1490
 GCTGCGTGGAAAGACTTGCAGCCGCTGCAGCGCCCGTGAACACGGCGCCACTTGC
 C V E D L R S R L Q R G P *

 1510 1530 1550
 CACCTAGGCGCTCTGGTGGCCCTTGAGAACCCCTAAGTACGGTTACTTATGCGTGTAGA

 1570 1590 1610
 CATTTTATGTCACTTATAAGCCGCTGGCACGGCCCTGCGTAGCAGCACCAAGCCGGCCCC

 1630 1650 1670
 ACCCCTGCTCGCCCCATCGCTCCAGCCAAGGCGAAGAACGACGAACGAATGTCGAGAGG

 1690 1710 1730
 GGGTGAAGACATTCTCAACTTCTCGGCCGGAGTTGGCTGAGATCGCGGTATTAAATCT

 1750 1770
 GTGAAAGAAAACAAAACAAAAACAAAAAAAAAAAAAAA

FIGURE 1B

1 ATGGAGCAGC GGCCGCGGGG CTGCGCGCG GTGGCGCGG CGCTCCCT CCT GGTGCTGCTG
 M E Q R P R G C A A V A A A L L L V L L
 61 GGGGCCCGGG CCCAGGGCGG CACTCGTAGC CCCAGGTGTG ACTGTGCCGG TGACTTCCAC
 G A R A Q G G T R S P R C D C A G D F H
 121 AAGAAGATTG GTCTGTTTTG TTGCAGAGGC TGCCCAGCGG GGCACATACCT GAAGGCCCC
 K K I G L F C C R G C P A G H Y L K A P
 181 TGCACGGAGC CCTGCGGCAA CTCCACCTGC CTTGTGTGTC CCCAAGACAC CTTCTTGCC
 C T E P C G N S T C L V C P Q D T F L A
 241 TGGGAGAAC ACCATAATTG TGAATGTGCC CGCTGCCAGG CCTGTGATGA GCAGGCCTCC
 W E N H H N S E C A R C Q A C D E Q A S
 301 CAGGTGGCGC TGGAGAACTG TTCAGCAGTG GCCGACACCC GCTGTGGCTG TAAGCCAGGC
 Q V A L E N C S A V A D T R C G C K P G
 361 TGGTTTGTGG AGTGCAGGT CAGCCAATGT GTCAGCAGTT CACCCCTCTA CTGCCAACCA
 W F V E C Q V S Q C V S S S P F Y C Q P
 421 TGCCTAGACT GCGGGGCCCT GCACCGCCAC ACACGGCTAC TCTGTCCCCG CAGAGATACT
 C L D C G A L H R H T R L L C S R R D T
 481 GACTGTGGGA CCTGCCTGCC TGGCTTCTAT GAACATGGCG ATGGCTGCGT GTCCTGCC
 D C G T C L P G F Y E H G D G C V S C P
 541 ACGAGCACCC TGGGGAGCTG TCCAGAGCGC TGTGCCGCTG TCTGTGGCTG GAGGCAGATG
 T S T L G S C P E R C A A V C G W R Q M
 601 TTCTGGTCC AGGTGCTCCT GGCTGGCTT GTGGTCCCCC TCCTGCTTGG GGCCACCTG
 F W V Q V L L A G L V V P L L L G A T L
 661 ACCTACACAT ACCGCCACTG CTGGCCTCAC AAGCCCCCTGG TTACTGCAGA TGAAGCTGGG
 T Y T Y R H C W P H K P L V T A D E A G
 721 ATGGAGGCTC TGACCCCCACC ACCGGCCACC CATCTGTACAC CCTTGGACAG CGCCACACC
 M E A L T P P P A T H L S P L D S A H T
 781 CTTCTAGCAC CTCCTGACAG CAGTGAGAAG ATCTGCACCG TCCAGTTGGT GGGTAACAGC
 L L A P P D S S E K I C T V Q L V G N S
 841 TGGACCCCTG GCTACCCCGA GACCCAGGAG GCGCTCTGCC CGCAGGTGAC ATGGTCC
 W T P G Y P E T Q E A L C P Q V T W S W
 901 GACCAGTTGC CCAGCAGAGC TCTTGGCCCC GCTGCTGCC CGCACACTCTC GCCAGAGTCC
 D Q L P S R A L G P A A A P T L S P E S
 961 CCAGCCGGCT CGCCAGCCAT GATGCTGCAG CCGGGCCCGC AGCTCTACGA CGTGATGGAC
 P A G S P A M M L Q P G P Q L Y D V M D
 1021 GCGGTCCCGAG CGCGCGCTG GAAGGAGTTG GTGCGCACGC TGGGGCTGCC CGAGGCAGAG
 A V P A R R W K E F V R T L G L R E A E
 1081 ATCGAAGCCG TGGAGGTGGA GATCGGCCGC TTCCGAGACC AGCAGTACGA GATGCTCAAG
 I E A V E V E I G R F R D Q Q Y E M L K
 1141 CGCTGGCGCC AGCAGCAGCC CGCGGGCCCTC GGAGCCGTTT ACGCAGCCCT GGAGCGCATG
 R W R Q Q Q P A G L G A V Y A A L E R M
 1201 GGGCTGGACG GCTGCCTGGA AGACTTGCGC AGCCGCCTGC AGCCGGCCCG GTGA
 G L D G C V E D L R S R L Q R G P

FIGURE 2

Consensus #1 M

DDCR	M E E T Q Q G E A P R G Q L R G E S A A P V P Q A L L L V L	30
TNFR1	M G L S T V P D L L L P L V L L E L L V G I Y P S G V I G L	30
FAS	M - L G I W T L L P L V L T S V A R L S S K S V N A Q V T D	29

Consensus #1 C

DDCR	L G A R A Q G G T R S P R C D C A G D F H - - K K I G L F C	58
TNFR1	V P H L G D R E K R D S V C P Q G K Y I H - - P Q N N S I C	58
FAS	I N S K G L E L R K T V T T V E T Q N L E G L H H D G Q F C	59

Consensus #1 . . . C . . . G C : C . . . C . . .

DDCR	C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T	88
TNFR1	C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S	88
FAS	H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K	89

Consensus #1 H C . . . C C

DDCR	F L A W E N H H N S E C A R C Q A C D E Q A S Q V A L E N C	118
TNFR1	F T A S E N H L R - H C L S C S K C R K E M G Q V E I S S C	117
FAS	E Y T D K A H F S S K C R R C R L C D E G H G L E V E I N C	119

Consensus #1 T . C . C

DDCR	S A V A D T R C G G C K P G W F V E C - - Q V S Q C V S S S	145
TNFR1	T V D R D T V C G G C R K N Q Y R H Y W S E N L F O C - - -	144
FAS	T R T Q N T K C R C K P N F F Q N - - - - - - - - - - - - -	137

Consensus #1 C

DDCR	P F Y C Q P C L D C G A L H R H T R L L C S R R D T D C G T	175
TNFR1	- F N C S L C L N - G T V H - - - L S C Q E K Q N T V C T	167
FAS	- - - S T V C E H C D P - - - - - - - - - C T K	148

Consensus #1 C . . . G C C . . .

DDCR	C L P G F Y E H G D G C V S C P T S T L G - S C P E R C - -	203
TNFR1	C C H A G F F L R E N E C V S C S N C K K S L E C T K L C L P	197
FAS	C E H G I I - - - K E C - - - - - T L T S N T K C - -	166

Consensus #1 L

DDCR	- - - - - A A V C G W R Q M F W V Q V L L A G L V V P L	225
TNFR1	Q I E N V K G T E D S G T V L L P L V I F F G L C L L S L	227
FAS	- - - - - K E E G S R S N L G W L C L L - - L P I P L	186

Consensus #1

DDCR	L L G G T L D L H I P P L L A H K P L V T A D E A G M E A L	255
TNFR1	L F I G - L M Y R Y Q R W K S K L Y S I V C G K S T P E K E	256
FAS	I V - - - - - - - - - W V K R K E V - - - Q K T C R K H R	203

Consensus #1 G P

DDCR	N P P P G T H L S P L D S A H T L L A P P D S S E K I C T V	285
TNFR1	G E L E G T T T K P L A P N P S F S P T P G F T P T L G F S	286
FAS	K E N Q G S H E S P - - - - - - - - - - - - - - - - - - -	214

FIGURE 3

Consensus #1

DDCR	Q L V G N S W	[P]	P G Y P E	[Q]	Q E A L	[C]	Q V T W S W D Q L -	315
TNFR1	P V P S S T F	[P]	S S S T Y	[P]	P G D -	[C]	N F A A P R R E V A	315
FAS	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	214

Consensus #1 L

DDCR	- [P] S R A L G	[P]	A A A P [T] L	S [P] E S P A G S - - - - -	336
TNFR1	P P Y Q G A D	[P]	I L A T A L A S D P I P N P	[L] Q K W E D S A	345
FAS	- - - - -	- - - - -	- [T] L N P E T V A I N E S - - - - -	226	

Consensus #1 K . F V

DDCR	- - - P A M M L Q P G P Q	[L]	D [V] M D A	[V] P A R R W K E F V	362	
TNFR1	H K P Q S L	[D]	T [D] D P A T	[L] Y A V V E N	V P P L R W K E F V	375
FAS	- - - - -	[D]	V D L S K Y I T T I A G V M T L S Q V K G F V	249		

Consensus #1 R . . G I L .

DDCR	R T [L] G L R E A B I E A V E V E I C R - F R D	[Q] Q Y E M L	K 391
TNFR1	R R [L] G L S D H E I D R L E L Q N G R C L R E A Q Y S M L	A 405	
FAS	R K N G V N E A K I D E I K N D N V Q D T A E Q K V Q L L R	279	

Consensus #1 . W A L L E

DDCR	R W R Q Q Q [P] - - - A G [L] G A V Y A A L E R M G L D	[G] G V [E]	418
TNFR1	T W R R R T P R R B A T L E L E G R V L R D M D L L C G C L E	435	
FAS	N W H Q L H G K K B A - Y D T L I K D L K K A N L C T L A E	308	

Consensus #1

DDCR	[D] L - - - - - R [S] R [L] Q R G [P]	428
TNFR1	[D] E E A L - - - - - C G P A A L P P A P S L [L] R	455
FAS	K [R] Q T I I L K D I T S D S E N S N F R N E I Q S [L] V	335

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '..'.

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIGURE 3 (CONT'D)

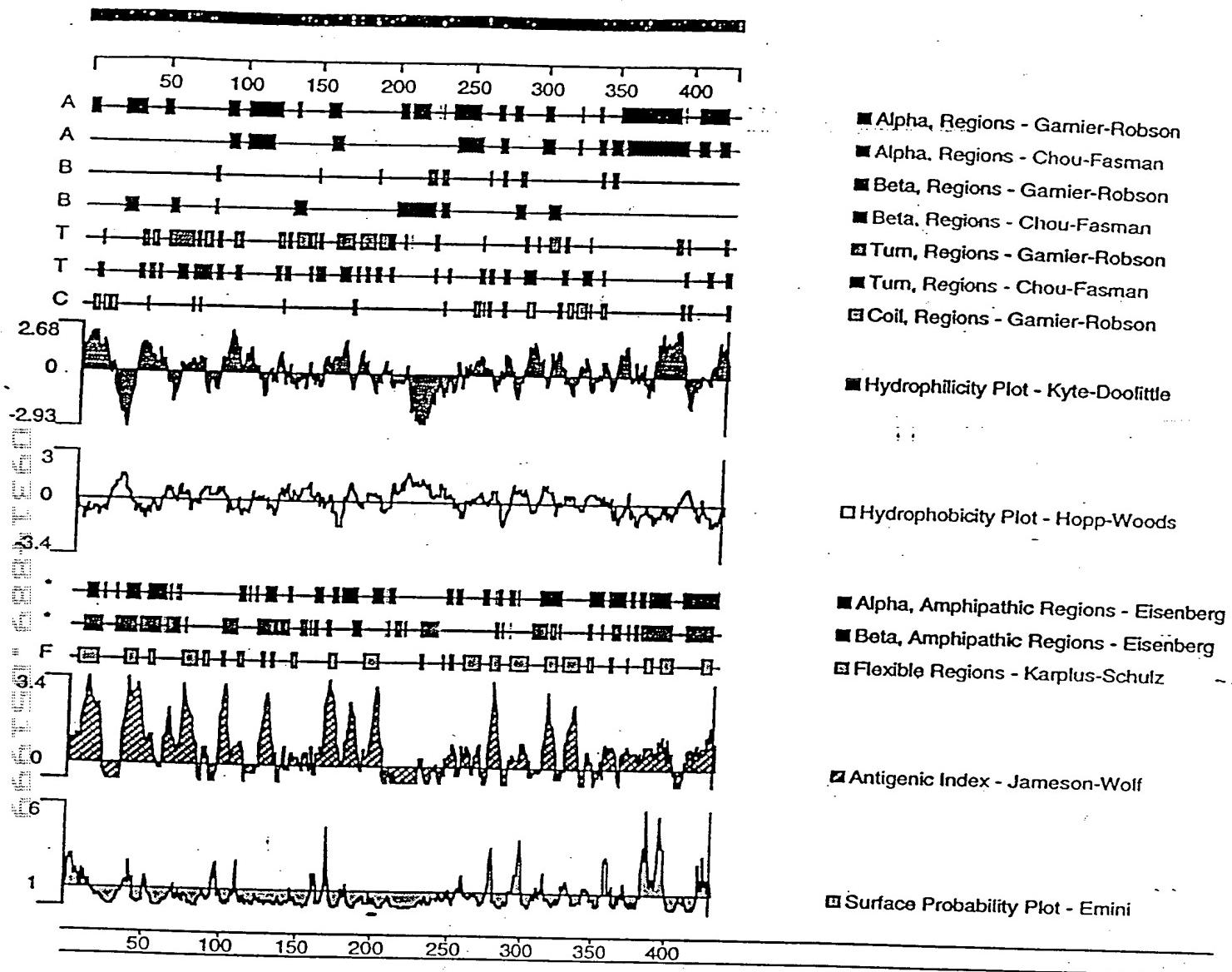


FIGURE 4